



1600

RAW SEQUENCE LISTING

DATE: 01/29/2004

PATENT APPLICATION: US/09/826,791A

TIME: 09:38:01

Input Set : A:\PC10914A Seq Listing 1-20-04.ST25.txt

Output Set: N:\CRF4\01292004\I826791A.raw

3 <110> APPLICANT: Pfizer Inc.
 4 Harland, Lee
 6 <120> TITLE OF INVENTION: Novel Polypeptide
 8 <130> FILE REFERENCE: PCS10914ADAM
 10 <140> CURRENT APPLICATION NUMBER: 09/826,791A
 11 <141> CURRENT FILING DATE: 2001-04-05
 13 <150> PRIOR APPLICATION NUMBER: 0008504.3
 14 <151> PRIOR FILING DATE: 2000-04-05
 16 <150> PRIOR APPLICATION NUMBER: 60/198,367
 17 <151> PRIOR FILING DATE: 2000-04-19
 19 <160> NUMBER OF SEQ ID NOS: 7
 21 <170> SOFTWARE: PatentIn version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 993
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1

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31	aagagagaat	ttttcccaat	tgtatatctg	ataatatatt	tctggggagt	cttgggaaat	120
33	gggttgtcca	tatatgtttt	cctgcagcct	tataagaagt	ccacatctgt	gaacgttttc	180
35	atgctaaatc	tggccatttc	agatctcctg	ttcataagca	cgtttccctt	cagggctgac	240
37	tattatctta	gaggctccaa	ttggatatatt	ggagacctgg	cctgcaggat	tatgtcttat	300
39	tccttgtatg	tcaacatgta	cagcagtatt	tatttcctga	ccgtgctgag	tgttgtgcgt	360
41	ttcctggcaa	tggttcaccc	ctttcggctt	ctgcatgtca	ccagcatcag	gagtgcctgg	420
43	atcctctgtg	ggatcatatg	gatccttatc	atggcttcct	caataatgct	cctggacagt	480
45	ggctctgagc	agaacggcag	tgtcacatca	tgcttagagc	tgaatctcta	taaaattgct	540
47	aagctgcaga	ccatgaacta	tattgccttg	gtggtgggct	gcctgctgcc	atttttcaca	600
49	ctcagcatct	gttatctgct	gatcattcgg	gttctgttaa	aagtggagggt	cccagaatcg	660
51	gggctgcggg	tttctcacag	gaaggcactg	accaccatca	tcatacctt	gatcatcttc	720
53	ttcttgtgtt	tcctgcccta	tcacacactg	aggaccgtcc	acttgacgac	atggaaagtg	780
55	ggtttatgca	aagacagact	gcataaagct	ttggttatca	cactggcctt	ggcagcagcc	840
57	aatgcctgct	tcaatcctct	gctctattac	tttgctgggg	agaattttta	ggacagacta	900
59	aagtctgcac	tcagaaaagg	ccatccacag	aaggcaaaga	caaagtgtgt	tttcctgtt	960
61	agtgtgtggt	tgagaaagga	aacaagagta	taa			993

64 <210> SEQ ID NO: 2
 65 <211> LENGTH: 330
 66 <212> TYPE: PRT
 67 <213> ORGANISM: Homo sapiens
 69 <400> SEQUENCE: 2

71	Met	Glu	Pro	Asn	Gly	Thr	Phe	Ser	Asn	Asn	Asn	Ser	Arg	Asn	Cys	Thr
72	1			5					10					15		
75	Ile	Glu	Asn	Phe	Lys	Arg	Glu	Phe	Phe	Pro	Ile	Val	Tyr	Leu	Ile	Ile
76				20					25					30		

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79 Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
80          35          40          45
83 Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
84          50          55          60
87 Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
88 65          70          75          80
91 Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
92          85          90          95
95 Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
96          100          105          110
99 Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
100          115          120          125
103 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
104          130          135          140
107 Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser
108 145          150          155          160
111 Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
112          165          170          175
115 Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
116          180          185          190
119 Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
120          195          200          205
123 Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
124          210          215          220
127 Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe
128 225          230          235          240
131 Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
132          245          250          255
135 Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val
136          260          265          270
139 Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu
140          275          280          285
143 Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu
144          290          295          300
147 Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val
148 305          310          315          320
151 Ser Val Trp Leu Arg Lys Glu Thr Arg Val
152          325          330
155 <210> SEQ ID NO: 3
156 <211> LENGTH: 24
157 <212> TYPE: DNA
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 3
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164 <210> SEQ ID NO: 4
165 <211> LENGTH: 22
166 <212> TYPE: DNA
167 <213> ORGANISM: Homo sapiens
169 <400> SEQUENCE: 4

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170 ttataactctt gtttcctttc tc 22
173 <210> SEQ ID NO: 5
174 <211> LENGTH: 1041
175 <212> TYPE: DNA
176 <213> ORGANISM: Homo sapiens
179 <220> FEATURE:
180 <221> NAME/KEY: CDS
181 <222> LOCATION: (1)..(1041)
183 <400> SEQUENCE: 5
184 atg gag aga aaa ttt atg tcc ttg caa cca tcc atc tcc gta tca gaa 48
185 Met Glu Arg Lys Phe Met Ser Leu Gln Pro Ser Ile Ser Val Ser Glu
186 1 5 10 15
188 atg gaa cca aat ggc acc ttc agc aat aac aac agc agg aac tgc aca 96
189 Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr
190 20 25 30
192 att gaa aac ttc aag aga gaa ttt ttc cca att gta tat ctg ata ata 144
193 Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile
194 35 40 45
196 ttt ttc tgg gga gtc ttg gga aat ggg ttg tcc ata tat gtt ttc ctg 192
197 Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
198 50 55 60
200 cag cct tat aag aag tcc aca tct gtg aac gtt ttc atg cta aat ctg 240
201 Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
202 65 70 75 80
204 gcc att tca gat ctc ctg ttc ata agc acg ctt ccc ttc agg gct gac 288
205 Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
206 85 90 95
208 tat tat ctt aga ggc tcc aat tgg ata ttt gga gac ctg gcc tgc agg 336
209 Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
210 100 105 110
212 att atg tct tat tcc ttg tat gtc aac atg tac agc agt att tat ttc 384
213 Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
214 115 120 125
216 ctg acc gtg ctg agt gtt gtg cgt ttc ctg gca atg gtt cac ccc ttt 432
217 Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
218 130 135 140
220 cgg ctt ctg cat gtc acc agc atc agg agt gcc tgg atc ctc tgt ggg 480
221 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
222 145 150 155 160
224 atc ata tgg atc ctt atc atg gct tcc tca ata atg ctc ctg gac agt 528
225 Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser
226 165 170 175
228 ggc tct gag cag aac ggc agt gtc aca tca tgc tta gag ctg aat ctc 576
229 Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
230 180 185 190
232 tat aaa att gct aag ctg cag acc atg aac tat att gcc ttg gtg gtg 624
233 Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
234 195 200 205
236 ggc tgc ctg ctg cca ttt ttc aca ctc agc atc tgt tat ctg ctg atc 672

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237 Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
238      210      215      220
240 att cgg gtt ctg tta aaa gtg gag gtc cca gaa tcg ggg ctg cgg gtt      720
241 Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
242 225      230      235      240
244 tct cac agg aag gca ctg acc acc atc atc atc acc ttg atc atc ttc      768
245 Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe
246      245      250      255
248 ttc ttg tgt ttc ctg ccc tat cac aca ctg agg acc gtc cac ttg acg      816
249 Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
250      260      265      270
252 aca tgg aaa gtg ggt tta tgc aaa gac aga ctg cat aaa gct ttg gtt      864
253 Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val
254      275      280      285
256 atc aca ctg gcc ttg gca gca gcc aat gcc tgc ttc aat cct ctg ctc      912
257 Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu
258      290      295      300
260 tat tac ttt gct ggg gag aat ttt aag gac aga cta aag tct gca ctc      960
261 Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu
262 305      310      315      320
264 aga aaa ggc cat cca cag aag gca aag aca aag tgt gtt ttc cct gtt      1008
265 Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val
266      325      330      335
268 agt gtg tgg ttg aga aag gaa aca aga gta taa      1041
269 Ser Val Trp Leu Arg Lys Glu Thr Arg Val
270      340      345
273 <210> SEQ ID NO: 6
274 <211> LENGTH: 346
275 <212> TYPE: PRT
276 <213> ORGANISM: Homo sapiens
278 <400> SEQUENCE: 6
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281 1      5      10      15
284 Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr
285      20      25      30
288 Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile
289      35      40      45
292 Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
293      50      55      60
296 Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
297 65      70      75      80
300 Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
301      85      90      95
304 Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
305      100      105      110
308 Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
309      115      120      125
312 Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
313      130      135      140

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316 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
317 145 150 155 160
320 Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser
321 165 170 175
324 Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
325 180 185 190
328 Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
329 195 200 205
332 Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
333 210 215 220
336 Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
337 225 230 235 240
340 Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe
341 245 250 255
344 Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
345 260 265 270
348 Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val
349 275 280 285
352 Ile Thr Leu Ala Leu Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu
353 290 295 300
356 Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu
357 305 310 315 320
360 Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val
361 325 330 335
364 Ser Val Trp Leu Arg Lys Glu Thr Arg Val
365 340 345
370 <210> SEQ ID NO: 7
371 <211> LENGTH: 674
372 <212> TYPE: PRT
373 <213> ORGANISM: Homo sapiens
375 <400> SEQUENCE: 7
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381 Thr Ile Asp Asp Phe Arg Asn Gln Val Tyr Ser Thr Leu Tyr Ser Met
382 20 25 30
385 Ile Ser Val Val Gly Phe Phe Gly Asn Gly Phe Val Leu Tyr Val Leu
386 35 40 45
389 Ile Lys Thr Tyr His Lys Lys Ser Ala Phe Gln Val Tyr Met Ile Asn
390 50 55 60
393 Leu Ala Val Ala Asp Leu Leu Cys Val Cys Thr Leu Pro Leu Arg Val
394 65 70 75 80
397 Val Tyr Tyr Val His Lys Gly Ile Trp Leu Phe Gly Asp Phe Leu Cys
398 85 90 95
401 Arg Leu Ser Thr Tyr Ala Leu Tyr Val Asn Leu Tyr Cys Ser Ile Phe
402 100 105 110
405 Phe Met Thr Ala Met Ser Phe Phe Arg Cys Ile Ala Ile Val Phe Pro
406 115 120 125
409 Val Gln Asn Ile Asn Leu Val Thr Gln Lys Lys Ala Arg Phe Val Cys
410 130 135 140

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VERIFICATION SUMMARY

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